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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2010; month=6; day=24; hr=8; min=21; sec=59; ms=301; ]

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Reviewer Comments:

<210> 1

<211> 3846

<212> DNA (BFA4 cDNA)

<213> Homo sapiens

Per 1.823 of the Sequence Rules, the above <212> response is invalid: the only valid <212> responses are just DNA, RNA, or PRT. All explanatory matter (which encompasses "BFA4 cDNA") goes in the <220>-<223> (Feature) section. See below for example:

<220>

<223> BFA4 cDNA

FYI: the above type of error also appears in Sequences 2-6.

<210> 105

<211> 16

<212> PRT

<213> Homo sapiens

<400> 105

Ser Arg Arg His His Cys Arg Ser Lys Ala Lys Arg Ser Arg His His

Please number the above amino acids under every 5 amino acids, starting with "1". Do not insert TAB codes between the amino acid numbers: TABs cause misaligned numbers. Use space characters, instead.

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Application No: 10553137 Version No: 2.0

Input Set:

Output Set:

Started: 2010-06-15 11:26:27.510  
Finished: 2010-06-15 11:26:29.386  
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 876 ms  
Total Warnings: 0  
Total Errors: 6  
No. of SeqIDs Defined: 105  
Actual SeqID Count: 105

Error code	Error Description
E 310	Invalid sequence type in <212> in SEQID: (1)
E 310	Invalid sequence type in <212> in SEQID: (2)
E 310	Invalid sequence type in <212> in SEQID: (3)
E 310	Invalid sequence type in <212> in SEQID: (4)
E 310	Invalid sequence type in <212> in SEQID: (5)
E 310	Invalid sequence type in <212> in SEQID: (6)

# SEQUENCE LISTING

<110> Berinstein, Neil  
Gallichan, Scott  
Lovitt, Corey  
Parrington, Mark  
Pedyczak, Artur  
Radvanyi, Laszlo  
Singh-Sandhu, Devender

<120> Tumor Antigens BFA5 for Prevention and/or Treatment of  
Cancer

<130> API-03-03-PCT-US

<140> 10553137

<141> 2010-06-15

<150> PCT/IB2004/001701

<151> 2004-04-15

<150> US 60/462,945

<151> 2003-04-15

<160> 105

<170> PatentIn version 3.2

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<212> DNA (BFA4 cDNA)

<213> Homo sapiens

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 <213> Homo sapiens

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Ser Asp Ala Ala Glu Leu Asn His Lys Glu Glu His Ser Leu His Val  
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Gln Asp Pro Ser Ser Ser Ser Lys Lys Asp Leu Lys Ser Ala Val Leu  
65 70 75 80

Ser Glu Lys Ala Gly Phe Asn Tyr Glu Ser Pro Ser Lys Gly Gly Asn  
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Phe Pro Ser Phe Pro His Asp Glu Val Thr Asp Arg Asn Met Leu Ala  
100 105 110

Phe Ser Phe Pro Ala Ala Gly Gly Val Cys Glu Pro Leu Lys Ser Pro  
115 120 125

Gln Arg Ala Glu Ala Asp Asp Pro Gln Asp Met Ala Cys Thr Pro Ser  
130 135 140

Gly Asp Ser Leu Glu Thr Lys Glu Asp Gln Lys Met Ser Pro Lys Ala  
145 150 155 160

Thr Glu Glu Thr Gly Gln Ala Gln Ser Gly Gln Ala Asn Cys Gln Gly  
165 170 175

Leu Ser Pro Val Ser Val Ala Ser Lys Asn Pro Gln Val Pro Ser Asp  
180 185 190

Gly Gly Val Arg Leu Asn Lys Ser Lys Thr Asp Leu Leu Val Asn Asp  
195 200 205

Asn Pro Asp Pro Ala Pro Leu Ser Pro Glu Leu Gln Asp Phe Lys Cys  
210 215 220

Asn Ile Cys Gly Tyr Gly Tyr Tyr Gly Asn Asp Pro Thr Asp Leu Ile  
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Lys His Phe Arg Lys Tyr His Leu Gly Leu His Asn Arg Thr Arg Gln  
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Asp Ala Glu Leu Asp Ser Lys Ile Leu Ala Leu His Asn Met Val Gln  
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Phe Ser His Ser Lys Asp Phe Gln Lys Val Asn Arg Ser Val Phe Ser  
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Gly Val Leu Gln Asp Ile Asn Ser Ser Arg Pro Val Leu Leu Asn Gly  
290 295 300

Thr Tyr Asp Val Gln Val Thr Ser Gly Gly Thr Phe Ile Gly Ile Gly  
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Arg Lys Thr Pro Asp Cys Gln Gly Asn Thr Lys Tyr Phe Arg Cys Lys  
325 330 335

Phe Cys Asn Phe Thr Tyr Met Gly Asn Ser Ser Thr Glu Leu Glu Gln  
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His Phe Leu Gln Thr His Pro Asn Lys Ile Lys Ala Ser Leu Pro Ser  
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Ser Glu Val Ala Lys Pro Ser Glu Lys Asn Ser Asn Lys Ser Ile Pro  
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Ala Leu Gln Ser Ser Asp Ser Gly Asp Leu Gly Lys Trp Gln Asp Lys  
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Tyr Tyr Trp Cys Lys Phe Cys Ser Phe Ser Cys Glu Ser Ser Ser Ser  
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His Ser Cys Tyr Lys Cys Arg Gln Cys Ser Phe Thr Ala Ala Asp Thr  
690 695 700

Gln Ser Leu Leu Glu His Phe Asn Thr Val His Cys Gln Glu Gln Asp  
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Ile Thr Thr Ala Asn Gly Glu Glu Asp Gly His Ala Ile Ser Thr Ile  
725 730 735

Lys Glu Glu Pro Lys Ile Asp Phe Arg Val Tyr Asn Leu Leu Thr Pro  
740 745 750

Asp Ser Lys Met Gly Glu Pro Val Ser Glu Ser Val Val Lys Arg Glu  
755 760 765

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770 775 780

Ser Ser Asp Asp Leu Arg Asn Val Thr Trp Arg Gly Ala Asp Ile Leu  
785 790 795 800

Arg Gly Ser Pro Ser Tyr Thr Gln Ala Ser Leu Gly Leu Leu Thr Pro  
805 810 815

Val Ser Gly Thr Gln Glu Gln Thr Lys Thr Leu Arg Asp Ser Pro Asn  
820 825 830

Val Glu Ala Ala His Leu Ala Arg Pro Ile Tyr Gly Leu Ala Val Glu  
835 840 845

Thr Lys Gly Phe Leu Gln Gly Ala Pro Ala Gly Gly Glu Lys Ser Gly  
850 855 860

Ala Leu Pro Gln Gln Tyr Pro Ala Ser Gly Glu Asn Lys Ser Lys Asp  
865 870 875 880

Glu Ser Gln Ser Leu Leu Arg Arg Arg Arg Gly Ser Gly Val Phe Cys  
885 890 895

Ala Asn Cys Leu Thr Thr Lys Thr Ser Leu Trp Arg Lys Asn Ala Asn

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Gln Arg Glu Ile Pro Leu Pro Ser Leu Ser Lys Tyr Glu Ala Gln Gly		
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